AMENDMENTS TO THE CLAIMS

1. (Currently Amended) An antisense oligonucleotide between 6 and about 50 bases in length comprising at least one non-naturally occurring backbone linkage ~~and between 6 and about 50 bases~~ and at least one degenerate or universal base, ~~wherein at least one of said bases are universal and/or degenerate bases and,~~ wherein said antisense oligonucleotide ~~complements~~ hybridizes to at least two RNA molecules that differ in sequence by at least one nucleotide mismatch, and wherein said degenerate or universal base of said antisense oligonucleotide is positioned on said antisense oligonucleotide to correspond to said nucleotide mismatch. ~~of a different sequence.~~

2. (Original) The antisense oligonucleotide of Claim 1, wherein no more than about 50% of said bases are universal and/or degenerate bases.

3. (Currently Amended) An antisense oligonucleotide comprising a first and a second non-RNase H recruiting region of between 3 and about 15 bases, and a ~~second non-~~RNase H recruiting region between 3 and about 15 bases, wherein at least one of said bases are universal and/or degenerate bases and, wherein said antisense oligonucleotide hybridizes to at least two RNA molecules that differ in sequence by at least one nucleotide mismatch, and wherein said degenerate or universal base of said antisense oligonucleotide is positioned on said antisense oligonucleotide to correspond to said nucleotide mismatch. ~~complements at least two RNA molecules of a different sequence.~~

4. (Original) The antisense oligonucleotide of Claim 3, wherein no more than about 50% of said bases are universal and/or degenerate bases.

5. (Currently Amended) An antisense oligonucleotide comprising an RNA targeting region, a non-RNase H recruiting ~~section~~ region and an RNase H recruiting ~~section~~region, wherein the RNA targeting region of said oligonucleotide comprises at least one ~~of said bases are~~ universal and/or degenerate bases and, wherein said antisense oligonucleotide ~~complements~~ hybridizes to at least two RNA molecules that differ in sequence by at least one nucleotide mismatch, and wherein said degenerate or universal base of said antisense oligonucleotide is positioned on said antisense oligonucleotide to correspond to said nucleotide mismatch. ~~of a different sequence.~~

6. (Currently Amended) The antisense oligonucleotide of Claim 5, wherein the RNA targeting region comprises no more than about 50% ~~of said bases are~~ universal and/or degenerate bases.

7. (Currently Amended) An antisense oligonucleotide comprising an RNA targeting region and ~~an~~ RNase L-recruiting region comprising a 2'-5' adenosine oligomer, wherein the RNA targeting region of said oligonucleotide comprises at least one universal and/or degenerate bases and, wherein said antisense oligonucleotide hybridizes to ~~complements~~ at least two RNA molecules that differ in sequence by at least one nucleotide mismatch, and wherein said degenerate or universal base of said antisense oligonucleotide is positioned on said antisense oligonucleotide to correspond to said nucleotide mismatch.~~of a different sequence.~~

8. (Original) The antisense oligonucleotide of Claim 7, wherein said RNA targeting region comprises no more than about 50% universal and/or degenerate bases.

9. (Currently Amended) An antisense oligonucleotide comprising an RNA targeting region and a ~~-~~RNase P recruiting region, wherein the RNA targeting region of said antisense oligonucleotide comprises at least one universal and/or degenerate bases and, wherein said antisense oligonucleotide ~~complements~~ hybridizes to at least two RNA molecules that differ in sequence by at least one nucleotide mismatch, and wherein said degenerate or universal base of said antisense oligonucleotide is positioned on said antisense oligonucleotide to correspond to said nucleotide mismatch. ~~of a different sequence.~~

10. (Original) The antisense oligonucleotide of Claim 9, wherein said RNA targeting region comprises no more than about 50% universal and/or degenerate bases.

11. (Currently Amended) A ribozyme comprising an RNA targeting region, which comprises at least one universal and/or degenerate bases, wherein said ~~antisense oligonucleotide~~ribozyme ~~complements~~ hybridizes to at least two RNA molecules that differ in sequence by at least one nucleotide mismatch, and wherein said degenerate or universal base of said ribozyme is positioned on said antisense oligonucleotide to correspond to said nucleotide mismatch.~~of a different sequence.~~

12. (Original) The ribozyme of Claim 11, wherein said RNA targeting region comprises no more than about 50% universal and/or degenerate bases.

13. (Withdrawn) A method for cleaving a plurality of target RNA molecules of different sequence, comprising contacting said target RNA molecules with an antisense

oligonucleotide according to any one of Claims 1-10 in the presence of an RNase capable of cleaving said target RNA molecules.

14. (Withdrawn) The method of Claim 13, wherein said RNase is selected from the group consisting of RNase H, RNase L, and RNase P.

15. (Withdrawn) A method for cleaving a plurality of target RNA molecules of different sequence, comprising contacting said target RNA molecules with a ribozyme according to Claims 11 or 12.

16. (Withdrawn) A method for cleaving a plurality of target RNA molecules of different sequenced, comprising contacting said target RNA molecules with an antisense oligonucleotide comprising between 6 and about 50 bases, wherein said antisense oligonucleotide comprises at least one universal and/or degenerate base and, wherein said antisense oligonucleotide complements at least two RNA molecules of a different sequence,

17. (Withdrawn) A method for reducing the deleterious effects of an antisense oligonucleotide comprising one or more sequence motifs, comprising replacing one or more bases within said one or more sequence motifs with one or more universal and/or degenerate bases.

18. (Withdrawn) The method of Claim 17, wherein said sequence motif is a CG dinucleotide.

19. (Withdrawn) The method of Claim 17, wherein said sequence motif is a poly-G sequence.

20. (New) The antisense oligonucleotide of claim 1 wherein said antisense oligonucleotide comprises one or more sequence motifs with one or more degenerate and/or universal base.

21. (New) The antisense oligonucleotide of claim 20 wherein said sequence motif is a CG dinucleotide.

22. (New) The antisense oligonucleotide of claim 20 wherein said sequence motif is a poly –G sequence.